

Fig. 1

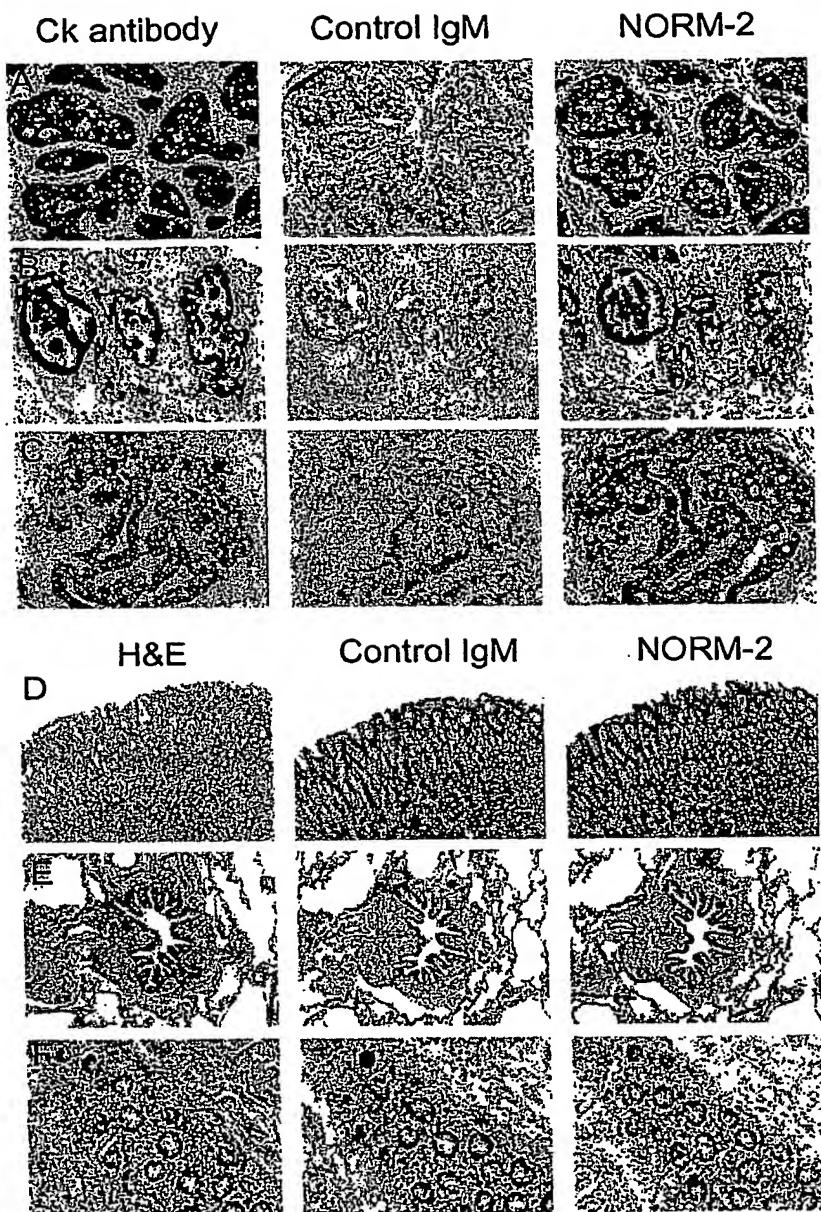


Fig. 2

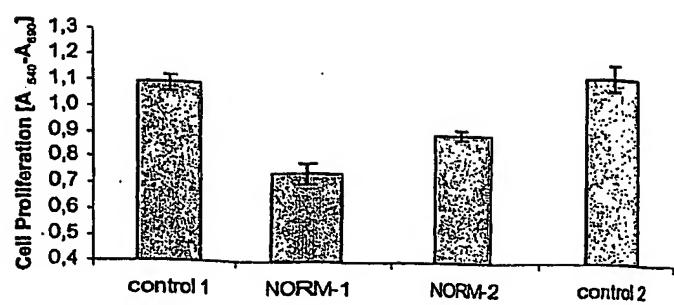


Fig. 3

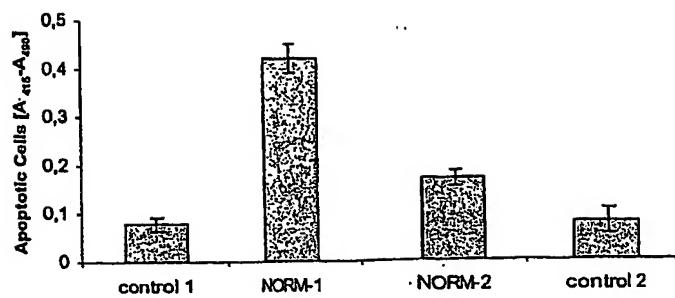


Fig. 4

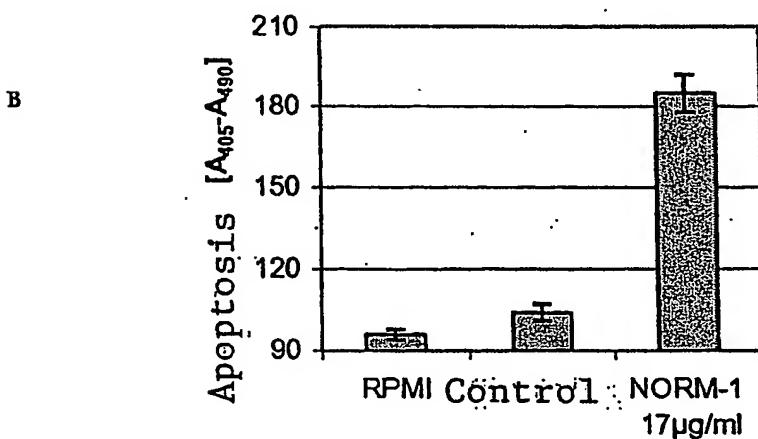
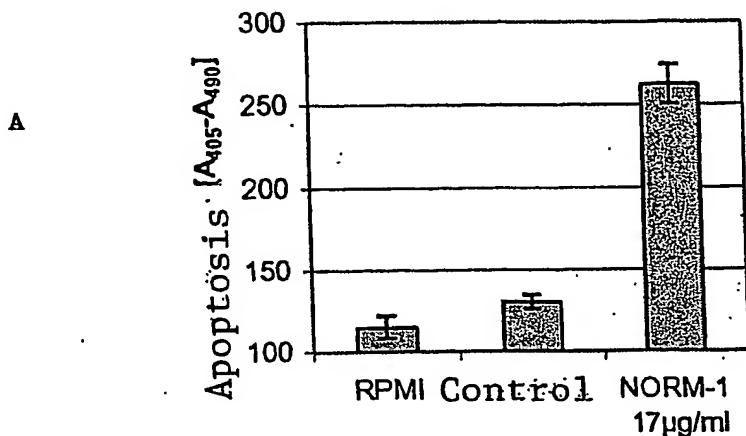


Fig. 5

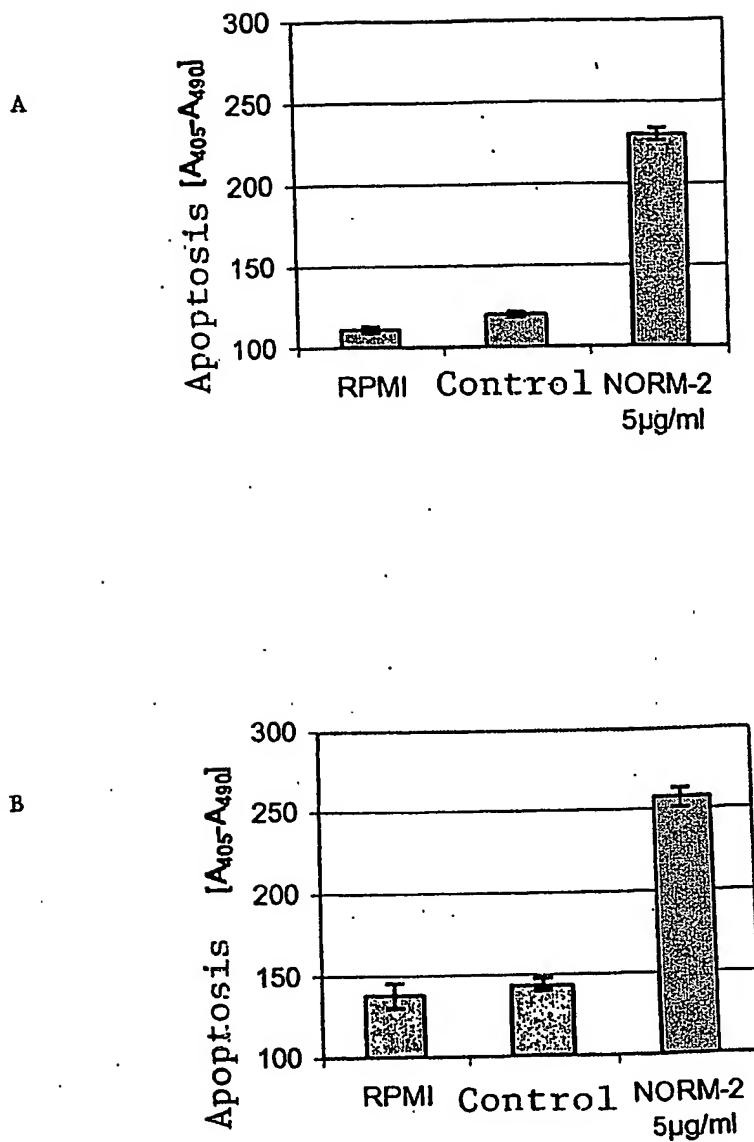


Fig. 6

NORM-1 (VH)

GAG GTG CAG CTG TRG GAG TCT GGG GGA GGC RTG GTA CAG CCT GGG TCC TAC AGA CTC	60
Glu Val Gln Leu Leu Glu Ser Gly Gly Leu Val Gln Pro Gly Ser Leu Arg Leu	
10 15 20	
1	
CDR1	
91 AGC TAT AGC AGC TAT AGC TAT AGC TCA GCT ATT AGT GGT AGT GGT GGT AGC ACA TAC TAC	105
TCC TGT GCA GCC TCT GGA TTC ACC TTT AGC AGC Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala	120
Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser 30 35 40	
CDR2	
148 CCA GGG AAG GGG CTG GAG TGG GTC TCA GCT ATT AGT GGT GGT GGT AGC ACA TAC TAC	180
CCA GGG AAG GGC CGG TTC ACC ATC TCC AGA GAC ATT TCC AAG AAC ACG CTG TAT	
Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Ser Thr Tyr Tyr Tyr	50 55 60
198	
GCA GAC TCC GTG AAG GGC CGG TTC ACC ATC TCC AGA GAC ATT TCC AAG AAC ACG CTG TAT	240
Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	70 75 80
65	
295	
CTG CAA ATG AAC AGC CTG AGA GCC GAG GAC ACG GCC GTA TAT TAC TGT GCG AAA GAT GGC	300
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Asp Gly	95 100
85 90	
321	
CDR3 D-Region	J-Region
TAT GAT AGT AGT GGT TAT TCG GAA TAT TAC TAC TAC TAC TAC ATG GAC GTC (SEQ. ID. NO: 2) 357	
Tyr Asp Ser Ser Gly Tyr Ser Glu Glu Tyr Tyr Tyr Tyr Met Asp Val (SEQ. ID. NO: 1) 115	110
105	

NORM-1 (VL)

TCC TAT GTG CTG ACT CAG CCA CCC TCG GTG TCA GTG TCC CCA GGA CAA ACG GCC AGG ATC  
 Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gln Thr Ala Arg Ile  
 1 5 10 15 20  
 CDR1 67 99 120  
 ACC TGC TCT GGA GAT GCA TGT CCA AAA AAA TAT GCT TAT TGG TAC CAG CAG AAG TCA GGG  
 Thr Cys Ser Gly Asp Ala Leu Pro Lys Lys Tyr Ala Tyr Trp Tyr Gln Gln Lys Ser Gly  
 25 30 35 40  
 CDR2 145 165 180  
 CAG GCC CCT GTG CTG GTC ATC TAT GAG GAC AGC AAA CGA CCC TCC GGG ATC CCT GAG AGA  
 Gln Ala Pro Val Leu Val Ile Tyr Glu Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg  
 45 50 55 60  
 J-Region 70 75 80  
 CDR3 262 297 300  
 TTC TCT GGC TCC AGC TCA GGG ACA ATG GCC ACC TTG ACT ATC AGT GGG GCC CAG GTG GAG  
 Phe Ser Gly Ser Ser Ser Gly Thr Met Ala Thr Leu Thr Ile Ser Gly Ala Gln Val Glu  
 65 70 75 80  
 J-Region 90 95 100  
 GAT GAA GCT GAC TAC TAC TGT TAC TCA ACA GAC AGC AGT GGT AAT CAT AGC TAT GTC TGC  
 Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Ser Gly Asn His Ser Tyr Val Phe (seq. ID. NO: 4) 300  
 85 90 95 100

NORM-2 (VH)

GAG GTG CAG CTG GTG GAG TCT GGG GGA GGC CTG GTC AAG CCT GGG GGG TCC TCC CTG AGA CTC Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg Leu 1 5 10 15 20			
1 5 10 15 20	91	CDR1	105
TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT AGC TAT AGC ATG AAC TGG GTC CGC CAG GCT Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ser Met Asn Trp Val Arg Gln Ala 25 30 35 40	148	CDR2	180
CCA GGG AAG GGG CTG GAG TGG GTC TCA TCC ATT AGT AGT TAC ATA TAC TAC Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Ser Ser Tyr Ile Tyr Tyr 45 50 55 60	198		240
GCA GAC TCA GTG AAG GGG CGA TTC ACC ATC TCC AGA GAC AAC GGC AAG AAC TCA CTG TAT Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr 65 70 75 80	295	D-Region	300
Leu Glu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg His Gly 85 90 95 100			
1 5 10 15 20	324	J-Region	324
CDR3			
AAC TAC TAC TAC TAC ATG GAC GTC (SEQ. ID. NO: 6) Asn Tyr Tyr Tyr Tyr Met Asp Val (SEQ. ID. NO: 5)			

Fig. 9:

NORM-2 (VL)

CAG TCT GTC TGT ACG CAG CCG CCC TCA GTG TCT GGG GCC CCA GGG CAG AGG GTC ACC ATC	60
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile	
1 5 10 15 20	
<u>67</u> CDR1	
TCC TGC ACT GGG AGC TCC AAC ATC GGG GCA GGT TAT GAT GTC CAC TGG TAC CAG CAG	108
Ser Cys Thr Gly Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val His Trp Tyr Gln Gln	
25 30 35 40	
<u>154</u> CDR2	
CCT CCA GGA ACA GCC CCC AAA CTC CTC ATC TAT GGT AAC AGC AAT CGG CCC TCA GGG GTC	174
Leu Pro Gly Thr Ala Pro Lys Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val	
45 50 55 60	
<u>271</u> CDR3	
CCT GAC CGG TTC TCT GGC TCC AAG TCT GGC ACC TCA GGC TCC TCG GCC ACT GGG CTC	240
Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu	
65 70 75 80	
J-Region	
CAG GCT GAG GAT GAG GCT GAT TAT TAC TGC CAG TCC TAT GAC AGC AGC CTG AGT GCC TTG	300
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser Leu Ser Ala Leu	
85 90 95 100	

303  
GTA TTC (seq. ID. no: 8)  
Val Phe (seq. ID. no: 7)

Fig. 10

**This Page is Inserted by IFW Indexing and Scanning  
Operations and is not part of the Official Record**

## **BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- BLACK BORDERS**
- IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**
- FADED TEXT OR DRAWING**
- BLURRED OR ILLEGIBLE TEXT OR DRAWING**
- SKEWED/SLANTED IMAGES**
- COLOR OR BLACK AND WHITE PHOTOGRAPHS**
- GRAY SCALE DOCUMENTS**
- LINES OR MARKS ON ORIGINAL DOCUMENT**
- REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY**
- OTHER:** \_\_\_\_\_

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.**